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TECH CENTER 1600/2900

1600

RAW SEQUENCE LISTING

DATE: 03/05/2003

PATENT APPLICATION: US/09/717,789B

TIME: 12:10:07

Input Set : A:\W168583.txt

Output Set: N:\CRF4\03052003\I717789B.raw

4 <110> APPLICANT: Chiorini, John
5 Kotin, Robert M.
6 Safer, Brian
8 <120> TITLE OF INVENTION: AAV5 VECTOR AND USES THEREOF
11 <130> FILE REFERENCE: 14014.0323U3
13 <140> CURRENT APPLICATION NUMBER: 09/717,789B
14 <141> CURRENT FILING DATE: 2000-11-21
17 <150> PRIOR APPLICATION NUMBER: PCT/US99/11958
18 <151> PRIOR FILING DATE: 1999-05-28
20 <150> PRIOR APPLICATION NUMBER: 60/087,029
21 <151> PRIOR FILING DATE: 1998-05-28
23 <160> NUMBER OF SEQ ID NOS: 24
25 <170> SOFTWARE: FastSEQ for Windows Version 3.0
27 <210> SEQ ID NO: 1
28 <211> LENGTH: 4652
29 <212> TYPE: DNA
30 <213> ORGANISM: Artificial Sequence
32 <220> FEATURE:
33 <223> OTHER INFORMATION: Description of Artificial Sequence:/Note =
34 synthetic construct
36 <400> SEQUENCE: 1

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40	gcgaacgcga caggggggag agtgccacac tctcaagcaa gggggttttg taagcagtga	180
41	tgtcataatg atgtaatgct tattgtcacg cgatagttaa tgattaacag tcatgtgatg	240
42	tgttttatcc aataggaaga aagcgcgcgt atgagttctc gcgagacttc cgggggtataa	300
43	aagaccgagt gaacgagccc gccgccattc tttgctctgg actgctagag gaccctcgct	360
44	gccatggcta ccttctatga agtcattggt cgcgtcccat ttgacgtgga ggaacatctg	420
45	cctggaattt ctgacagctt tgtggactgg gtaactggtc aaatttgga gctgcctcca	480
46	gagtcagatt taaatttgac tctggttgaa cagcctcagt tgacggtggc tgatagaatt	540
47	cgccgcgtgt tcctgtacga gtggaacaaa ttttccaagc aggagtccaa attctttgtg	600
48	cagtttgaaa aggatctga atattttcat ctgcacacgc ttgtggagac ctccggcatc	660
49	tcttccatgg tcctcggccg ctacgtgagt cagattcgcg ccagctggt gaaagtggtc	720
50	ttccagggaa ttgaaccca gatcaacgac tgggtcgcca tcaccaaggt aaagaagggc	780
51	ggagccaata agtggtgga ttctgggtat attccgcct acctgtgcc gaaggtccaa	840
52	ccggagcttc agtgggcgtg gacaaacctg gacgagtata aattggccgc cctgaatctg	900
53	gaggagcgca aacggctcgt cgcgcagttt ctggcagaat cctcgacgag ctcgcaggag	960
54	gcggcttcgc agcgtgagtt ctcggctgac ccggtcatca aaagcaagac ttcccagaaa	1020
55	tacatggcgc tcgtcaactg gctcgtggag caccgcatca cttccgagaa gcagtggatc	1080
56	caggaaaatc aggagagcta cctctccctc aactccaccg gcaactctcg gagccgatc	1140
57	aaggccgcgc tcgacaacgc gaccaaattt atgagtctga caaaaagcgc ggtggactac	1200
58	ctcgtgggga gctccgttcc cgaggacatt tcaaaaaaca gaatctggca aatttttgag	1260
59	atgaatggct acgacccggc ctacgcggga tccatcctct acggctggtg tcagcgctcc	1320

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61	gcggaggcca	tcgcccacac	tgtgcccttt	tacggctgcg	tgaactggac	caatgaaaac	1440
62	tttcccttta	atgactgtgt	ggacaaaatg	ctcatttggt	gggaggagg	aaagatgacc	1500
63	aacaaggtgg	ttgaatccgc	caaggccatc	ctggggggct	caaaggtgcg	ggtcgatcag	1560
64	aaatgtaaat	cctctgttca	aattgattct	acccctgtca	ttgtaacttc	caatacaaac	1620
65	atgtgtgtgg	tgggtgatgg	gaattccacg	acctttgaac	accagcagcc	gctggaggac	1680
66	cgcatgttca	aatttgaact	gactaagcgg	ctcccgccag	attttggcaa	gattactaag	1740
67	caggaagtca	aggacttttt	tgcttgggca	aagggtcaatc	aggtgccggg	gactcacgag	1800
68	tttaaagtgc	ccagggaatt	ggcgggaact	aaagggggcg	agaaatctct	aaaacgcccc	1860
69	ctgggtgacg	tcaccaatac	tagctataaa	agtctggaga	agcgggccag	gctctcattt	1920
70	gttcccagag	cgctcgcag	ttcagacgtg	actgttgatc	ccgctcctct	gcgaccgctc	1980
71	aattggaatt	caaggtatga	ttgcaaattg	gactatcatg	ctcaatttga	caacatttct	2040
72	aacaaatgtg	atgaatgtga	atatttgaat	cggggcaaaa	atggatgtat	ctgtcacaaat	2100
73	gtaactcact	gtcaaatttg	tcatgggatt	ccccctggg	aaaaggaaaa	cttgtcagat	2160
74	tttggggatt	ttgacgatgc	caataaagaa	cagtaaataa	agcgagtagt	catgtctttt	2220
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76	cttgaagcgg	gcccaccgaa	acaaaaaccc	aatcagcagc	atcaagatca	agcccgtggg	2340
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82	atagacgacc	actttccaaa	aagaaagaag	gctcggaccg	aagaggactc	caagccttcc	2700
83	acctcgtcag	acgccgaagc	tggaccacgc	ggatcccagc	agctgcaaat	cccagcccaa	2760
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86	tggatggggg	acagagtcgt	caccaagtcc	acccgaacct	gggtgctgcc	cagctacaac	2940
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88	tttgataca	gcacccctcg	gggtactttt	gactttaacc	gcttccacag	ccactggagc	3060
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90	gtcaaaatct	tcaacattca	agtcaaagag	gtcacgggtg	aggactccac	caccaccatc	3180
91	gccaacaacc	tcacctccac	cgtccaagtg	tttacggacg	acgactacca	gctgccctac	3240
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93	ccgcagtacg	gttacgcgac	gctgaaccgc	gacaacacag	aaaatcccac	cgagaggagc	3360
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101	gagaactact	tgatcttcaa	cagccagccg	gcgaacccgg	gcaccaccgc	cacgtacctc	3840
102	gagggaaca	tgctcatcac	cagcgagagc	gagacgcagc	cggtgaaccg	cgtggcgtag	3900
103	aacgtcggcg	ggcagatggc	caccaacaac	cagagctcca	ccactgcccc	cgcgaccggc	3960
104	acgtacaacc	tccaggaaat	cgtgcccggc	agcgtgtgga	tggagaggga	cgtgtacctc	4020
105	caaggaccca	tctgggcca	gatcccagag	acggggggcg	actttcacc	ctctccggcc	4080
106	atgggcggat	tcgactcaa	acacccaccg	ccatgatgc	tcatcaagaa	cacgcctgtg	4140
107	cccgaaata	tcaccagctt	ctcggacgtg	cccgtcagca	gcttcatcac	ccagtagcgc	4200
108	accgggcagg	tcaccgtgga	gatggagtgg	gagctcaaga	aggaaaactc	caagaggtgg	4260

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109 aacccagaga tccagtagac aaacaactac aacgaccccc agtttgtgga ctttgccccg 4320
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111 ctttaacca ttcattgtcg ataccctcaa taaaccgtgt attcgtgtca gtaaaatact 4440
112 gcctcttgtg gtcattcaat gaataacagc ttacaacatc tacaaaacct ctttgcttga 4500
113 gagtgtggca ctctcccccc tgctcgcttc gctcgctcgc tggctcgttt gggggggtgg 4560
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125 <220> FEATURE:
126 <223> OTHER INFORMATION: Description of Artificial Sequence:/Note =
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129 <400> SEQUENCE: 2
131 Met Ala Leu Val Asn Trp Leu Val Glu His Gly Ile Thr Ser Glu Lys
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133 Gln Trp Ile Gln Glu Asn Gln Glu Ser Tyr Leu Ser Phe Asn Ser Thr
134           20           25           30
135 Gly Asn Ser Arg Ser Gln Ile Lys Ala Ala Leu Asp Asn Ala Thr Lys
136           35           40           45
137 Ile Met Ser Leu Thr Lys Ser Ala Val Asp Tyr Leu Val Gly Ser Ser
138           50           55           60
139 Val Pro Glu Asp Ile Ser Lys Asn Arg Ile Trp Gln Ile Phe Glu Met
140           65           70           75           80
141 Asn Gly Tyr Asp Pro Ala Tyr Ala Gly Ser Ile Leu Tyr Gly Trp Cys
142           85           90           95
143 Gln Arg Ser Phe Asn Lys Arg Asn Thr Val Trp Leu Tyr Gly Pro Ala
144           100          105          110
145 Thr Thr Gly Lys Thr Asn Ile Ala Glu Ala Ile Ala His Thr Val Pro
146           115          120          125
147 Phe Tyr Gly Cys Val Asn Trp Thr Asn Glu Asn Phe Pro Phe Asn Asp
148           130          135          140
149 Cys Val Asp Lys Met Leu Ile Trp Trp Glu Glu Gly Lys Met Thr Asn
150           145          150          155          160
151 Lys Val Val Glu Ser Ala Lys Ala Ile Leu Gly Gly Ser Lys Val Arg
152           165          170          175
153 Val Asp Gln Lys Cys Lys Ser Ser Val Gln Ile Asp Ser Thr Pro Val
154           180          185          190
155 Ile Val Thr Ser Asn Thr Asn Met Cys Val Val Val Asp Gly Asn Ser
156           195          200          205
157 Thr Thr Phe Glu His Gln Gln Pro Leu Glu Asp Arg Met Phe Lys Phe
158           210          215          220
159 Glu Leu Thr Lys Arg Leu Pro Pro Asp Phe Gly Lys Ile Thr Lys Gln
160           225          230          235          240
161 Glu Val Lys Asp Phe Phe Ala Trp Ala Lys Val Asn Gln Val Pro Val
162           245          250          255
163 Thr His Glu Phe Lys Val Pro Arg Glu Leu Ala Gly Thr Lys Gly Ala
164           260          265          270

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165  Glu Lys Ser Leu Lys Arg Pro Leu Gly Asp Val Thr Asn Thr Ser Tyr
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168          290                      295                      300
169  Arg Ser Ser Asp Val Thr Val Asp Pro Ala Pro Leu Arg Pro Leu Asn
170  305                      310                      315                      320
171  Trp Asn Ser Arg Tyr Asp Cys Lys Cys Asp Tyr His Ala Gln Phe Asp
172          325                      330                      335
173  Asn Ile Ser Asn Lys Cys Asp Glu Cys Glu Tyr Leu Asn Arg Gly Lys
174          340                      345                      350
175  Asn Gly Cys Ile Cys His Asn Val Thr His Cys Gln Ile Cys His Gly
176          355                      360                      365
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184 <211> LENGTH: 610
185 <212> TYPE: PRT
186 <213> ORGANISM: Artificial Sequence
188 <220> FEATURE:
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196  Glu His Leu Pro Gly Ile Ser Asp Ser Phe Val Asp Trp Val Thr Gly
197          20          25          30
198  Gln Ile Trp Glu Leu Pro Pro Glu Ser Asp Leu Asn Leu Thr Leu Val
199          35          40          45
200  Glu Gln Pro Gln Leu Thr Val Ala Asp Arg Ile Arg Arg Val Phe Leu
201          50          55          60
202  Tyr Glu Trp Asn Lys Phe Ser Lys Gln Glu Ser Lys Phe Phe Val Gln
203  65          70          75          80
204  Phe Glu Lys Gly Ser Glu Tyr Phe His Leu His Thr Leu Val Glu Thr
205          85          90          95
206  Ser Gly Ile Ser Ser Met Val Leu Gly Arg Tyr Val Ser Gln Ile Arg
207          100         105         110
208  Ala Gln Leu Val Lys Val Val Phe Gln Gly Ile Glu Pro Gln Ile Asn
209          115         120         125
210  Asp Trp Val Ala Ile Thr Lys Val Lys Lys Gly Gly Ala Asn Lys Val
211          130         135         140
212  Val Asp Ser Gly Tyr Ile Pro Ala Tyr Leu Leu Pro Lys Val Gln Pro
213  145         150         155         160
214  Glu Leu Gln Trp Ala Trp Thr Asn Leu Asp Glu Tyr Lys Leu Ala Ala
215          165         170         175
216  Leu Asn Leu Glu Arg Lys Arg Leu Val Ala Gln Phe Leu Ala Glu
217          180         185         190
218  Ser Ser Gln Arg Ser Gln Glu Ala Ala Ser Gln Arg Glu Phe Ser Ala

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222	Asn	Trp	Leu	Val	Glu	His	Gly	Ile	Thr	Ser	Glu	Lys	Gln	Trp	Ile	Gln
223	225					230					235				240	
224	Glu	Asn	Gln	Glu	Ser	Tyr	Leu	Ser	Phe	Asn	Ser	Thr	Gly	Asn	Ser	Arg
225					245					250					255	
226	Ser	Gln	Ile	Lys	Ala	Ala	Leu	Asp	Asn	Ala	Thr	Lys	Ile	Met	Ser	Leu
227				260					265					270		
228	Thr	Lys	Ser	Ala	Val	Asp	Tyr	Leu	Val	Gly	Ser	Ser	Val	Pro	Glu	Asp
229			275					280					285			
230	Ile	Ser	Lys	Asn	Arg	Ile	Trp	Gln	Ile	Phe	Glu	Met	Asn	Gly	Tyr	Asp
231		290				295						300				
232	Pro	Ala	Tyr	Ala	Gly	Ser	Ile	Leu	Tyr	Gly	Trp	Cys	Gln	Arg	Ser	Phe
233	305					310					315				320	
234	Asn	Lys	Arg	Asn	Thr	Val	Trp	Leu	Tyr	Gly	Pro	Ala	Thr	Thr	Gly	Lys
235				325						330					335	
236	Thr	Asn	Ile	Ala	Glu	Ala	Ile	Ala	His	Thr	Val	Pro	Phe	Tyr	Gly	Cys
237				340					345					350		
238	Val	Asn	Trp	Thr	Asn	Glu	Asn	Phe	Pro	Phe	Asn	Asp	Cys	Val	Asp	Lys
239		355					360					365				
240	Met	Leu	Ile	Trp	Trp	Glu	Glu	Gly	Lys	Met	Thr	Asn	Lys	Val	Val	Glu
241		370					375					380				
243	Ser	Ala	Lys	Ala	Ile	Leu	Gly	Gly	Ser	Lys	Val	Arg	Val	Asp	Gln	Lys
244	385					390					395				400	
245	Cys	Lys	Ser	Ser	Val	Gln	Ile	Asp	Ser	Thr	Pro	Val	Ile	Val	Thr	Ser
246				405						410					415	
247	Asn	Thr	Asn	Met	Cys	Val	Val	Val	Asp	Gly	Asn	Ser	Thr	Thr	Phe	Glu
248			420						425					430		
249	His	Gln	Gln	Pro	Leu	Glu	Asp	Arg	Met	Phe	Lys	Phe	Glu	Leu	Thr	Lys
250		435						440					445			
251	Arg	Leu	Pro	Pro	Asp	Phe	Gly	Lys	Ile	Thr	Lys	Gln	Glu	Val	Lys	Asp
252		450					455					460				
253	Phe	Phe	Ala	Trp	Ala	Lys	Val	Asn	Gln	Val	Pro	Val	Thr	His	Glu	Phe
254	465					470					475				480	
255	Lys	Val	Pro	Arg	Glu	Leu	Ala	Gly	Thr	Lys	Gly	Ala	Glu	Lys	Ser	Leu
256				485						490					495	
257	Lys	Arg	Pro	Leu	Gly	Asp	Val	Thr	Asn	Thr	Ser	Tyr	Lys	Ser	Leu	Glu
258			500						505					510		
259	Lys	Arg	Ala	Arg	Leu	Ser	Phe	Val	Pro	Glu	Thr	Pro	Arg	Ser	Ser	Asp
260		515						520					525			
261	Val	Thr	Val	Asp	Pro	Ala	Pro	Leu	Arg	Pro	Leu	Asn	Trp	Asn	Ser	Arg
262		530					535						540			
263	Tyr	Asp	Cys	Lys	Cys	Asp	Tyr	His	Ala	Gln	Phe	Asp	Asn	Ile	Ser	Asn
264	545					550					555				560	
265	Lys	Cys	Asp	Glu	Cys	Glu	Tyr	Leu	Asn	Arg	Gly	Lys	Asn	Gly	Cys	Ile
266				565						570					575	
267	Cys	His	Asn	Val	Thr	His	Cys	Gln	Ile	Cys	His	Gly	Ile	Pro	Pro	Trp
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L:1111 M:283 W: Missing Blank Line separator, <220> field identifier